SEQUENCE

SEQ ID NO: 1

Sequence Length: 780

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Sequence :												
TGGTGAAGCT CTAACGGCTG TTTTGACTGG CGTAGCCGGA GCCGGCGACG TGAGGCGGGC												
STTGCTCGCG CGACAAGTAG TTGCTGGGAC AGCGAA ATG GAG GGG TGT GTG TCT 114	4											
Met Glu Gly Cys Val Ser												
1 5												
AAC CTA ATG GTC TGC AAC CTG GCC TAC AGC GGG AAG CTG GAA GAG TTG 163	2											
Asn Leu Met Val Cys Asn Leu Ala Tyr Ser Gly Lys Leu Glu Glu Leu												
10 15 20												
aag gag agt att ctg gcc\xat aaa tcc ctg gct act aga act gac cag 210	0											
Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu Ala Thr Arg Thr Asp Gln												
25 \30 \ 35												
GAC AGC AGA ACT GCA TTG CAC TGG GCA TGC TCA GCT GGA CAT ACA GAA 250	3											
Asp Ser Arg Thr Ala Leu His Trp Ala Cys Ser Ala Gly His Thr Glu												
40 45 50												
ATT GTT GAA TTT TTG TTG CAA CTT GGA GTG CCA GTG AAT GAT AAA GAC 30	6											
Ile Val Glu Phe Leu Leu Gln Leu Gly Val Pro Val Asn Asp Lys Asp												
55 60 65 70												
GAT GCA GGT TGG TCT CCT CTT CAT ATT GCG GCT TCT GCT GGC CGG GAT 35	4											
Asp Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp												
75 80 85												
GAG ATT GTA AAA GCC CTT CTG GGA AAA GGT GCT CAA GTG\AAT GCT GTC 40%	2											
Glu Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val												
90 95 . 100												
AAT CAA AAT GGC TGT ACT CCC TTA CAT TAT GCA GCT TCG AAA AAC AGG 450	0											
Asn Gln Asn Gly Cys Thr Pro Leu His Tyr Ala Ala Ser Lys Ash Arg												
105 110 115												
CAT GAG ATC GCT GTC ATG TTA CTG GAA GGC GGG GCT AAT CCA GAT GCT 490	В											
His Glu Ile Ala Val Met Leu Leu Glu Gly Gly Ala Asn Pro Asp Ala												
120 125 130												

AAG	GAC	CAT	TAT	GAG	GCT	ACA	GCA	ATG	CAC	CGG	GCA	GCA	GCC	AAG	GGT	546
Lys	Asp	His	Tyr	Glu	Ala	Thr	Ala	Met	His	Arg	Ala	Ala	Ala	Lys	${ t Gly}$	
135					140					145					150	
AAC	TTG	AAG	ATG	ATT	CAT	ATC	CTT	CTG	TAC	TAC	AAA	GCA	TCC	ACA	AAC	594
Asn	Leu	Lys	Met	Ile	His	Ile	Leu	Leu	Tyr	Tyr	Lys	Ala	Ser	Thr	Asn	
				155					160					165		
ATC	CAA	GAC	ACT	GAG	GGT	AAC	ACT	CCT	CTA	CAC	TTA	GCC	TGT	GAT	GAG	642
Ile	Gln	Asp	Thr	Glu	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Asp	Glu	
			170					175					180			
GAG	AGA	GTG	GAA	GAA	GCA	AAA	CTG	CTG	GTG	TCC	CAA	GGA	GCA	AGT	ATT	690
Glu	Arg	Val	Glu	Glu	Ala	Lys	Leu	Leu	Val	Ser	Gln	Gly	Ala	Ser	Ile	
		185					190					195				
TAC	ATT	GAG	AAT	AAA	GAA	GAA	AAG	ACA	CCC	CTG	CAA	GTG	GCC	AAA	GGT	738
Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	Leu	Gln	Val	Ala	Lys	Gly	
	200					205					210					
GGC	CTG	GGT	TTA	ATA	CTC	AAG	AGA	ATG	GTG	GAA	GGT	TAA	ACA			780
Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Met	Val	Glu	Gly					
215					220					225						

SEQ ID NO: 2

Sequence Length: 226

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Protein

Sequence

Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Ser 5 10 Gly Lys Leu Glu Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu 25 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys 40 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val 55 60 Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala 70 75 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Gly Lys Gly 85 90

Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr

100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly 115 120 Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Glu Ala Thr Ala Met His 135 Arg Ala Ala Lys Gly Asn Leu Lys Met Ile His Ile Leu Leu Tyr 145 150 155 160 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu 165 170 His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Val 180 185 190 Ser Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro 200 Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Met Val 210 215 220 Glu Gly 225 SEQ ID NO: Sequence Length: 693 Sequence Type: Nucleic acid Strandedness: Double Topology: Linear Molecular Type: cDNA Sequence ATG GAG GGG TGT GTG TCT AAC ATA ATG ATC TGT AAC CTG GCC TAC AGT 48 Met Glu Gly Cys Val Ser Asn Ile Met Ile Cys Asn Leu Ala Tyr Ser 5 10

GGG AAG CTG GAT GAG TTG AAG GAG CGC ATT TTG GCT GAT AAA TCT CTG 96 Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu 20 25 GCT ACT AGA ACT GAT CAG GAC AGC AGA ACA GCT TTG CAC TGG GCA TGC 144 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys 35 40 45 TCA GCT GGC CAT ACA GAA ATT GTT GAA TTC TTG CTG CAA CTT GGA GTG 192 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val 50 55 60

CCA	GTN	AAT	GAT	AAA	GAT	GAC	GCA	GGT	TGG	TCT	CCT	CTT	CAT	ATT	GCT	240
Pro	Val	Asn	Asp	Lys	Asp	Asp	Ala	Gly	Trp	Ser	Pro	Leu	His	Ile	Ala	
65					70					75					80	
GCC	TCC	GCT	GGC	CGG	GAT	GAG	ATT	GTA	AAA	GCC	CTT	CTG	GTG	AAA	GGT	288
Ala	Ser	Ala	Gly	Arg	Asp	Glu	Ile	Val	Lys	Ala	Leu	Leu	Val	Lys	Gly	
				85					90					95		
GCA	CAT	GTT	AAT	TCT	GTC	AAT	CAA	AAC	GGC	TGC	ACT	CCA	CTC	CAT	TAT	336
Ala	His	Val	Asn	Ser	Val	Asn	Gln	Asn	Gly	Cys	Thr	Pro	Leu	His	Tyr	
			100					105					110			
GCA	GCT	TCG	AAG	AAT	AGG	CAT	GAG	ATT	TCT	GTT	ATG	TTA	CTA	GAA	GGT	384
Ala	Ala	Ser	Lys	Asn	Arg	His	Glu	Ile	Ser	Val	Met	Leu	Leu	Glu	Gly	
		115					120					125				
GGG	GCT	AAC	CCA	GAT	GCG	AAG	GAC	CAT	TAC	GAT	GCT	ACA	GCA	ATG	CAC	432
Gly	Ala	Asn	Pro	Asp	Ala	Lys	Asp	His	Tyr	Asp	Ala	Thr	Ala	Met	His	
	130					135					140					
CGG	GCA	GCA	GCC	AAG	GGT	AAC	TTG	AAG	ATG	GTT	CAC	ATC	CTT	CTG	TTC	480
Arg	Ala	Ala	Ala	Lys	Gly	Asn	Leu	Lys	Met	Val	His	Ile	Leu	Leu	Phe	
145					150					155					160	
TAC	AAA	GCA	TCC	ACA	AAC	ATC	CAA	GAC	ACT	GAG	GGT	AAC	ACT	CCT	CTA	528
Tyr	Lys	Ala	Ser	Thr	Asn	Ile	Gln	Asp	Thr	Glu	Gly	Asn	Thr	Pro	Leu	
				165					170					175		
CAC	TTA	GCC	TGT	GAT	GAA	GAG	AGA	GTG	GAA	GAG	GCA	AAA	TTT	CTG	GTG	576
His	Leu	Ala	Суз	Asp	Glu	Glu	Arg	Val	Glu	Glu	Ala	Lys	Phe	Leu	Val	
			180					185					190			
ACT	CAA	GGA	GCA	AGT	ATT	TAC	ATT	GAG	TAA	AAA	GAA	GAA	AAG	ACA	CCC	624
Thr	Gln	Gly	Ala	Ser	Ile	Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	
		195					200					205				
CTG	CAA	GTT	GCC	AAA	GGG	GGC	CTG	GGT	TTA	ATA	CTC	AAG	AGA	CTA	GCA	672
Leu	Gln	Val	Ala	Lys	Gly	Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Leu	Ala	
	210					215					220					
						ATG	TAG									720
	Ser	Glu	Glu	Ala		Met										
225					230											

SEQ ID NO: 4

Sequence Length: 231

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Protein

Sequence

Met Glu Gly Cys Val Ser Asn Ile Met Ile Cys Asn Leu Ala Tyr Ser

1 5 10 15

Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu
20 25 30

Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
35 40 45

Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
50 55 60

Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
65 70 75 80

Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly
85 90 95

Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly
115 120 125

Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His
130 135 140

Arg Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe 145 150 155 160

Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
165 170 175

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val 180 185 190

Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro 195 200 205

Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala 210 215 220

Glu Ser Glu Glu Ala Ser Met

225 230

SEQ ID NO: 5

Sequence Length: 693

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Sequence ATG GAG GGG TGT GTG TCT AAC CTA ATG GTC TGT AAC CTG GCC TAC AAC 48 Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Asn GGG AAG CTG GAT GAG TTG AAG GAA AGC ATT TTG GCT GAT AAG TCT CTG 96 Gly Lys Leu Asp Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu 20 25 30 GCC ACT AGA ACT GAT CAG GAC AGC AGA ACA GCA TTG CAC TGG GCA TGC 144 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys 35 TCA GCT GGT CAT ACA GAA ATT GTT GAA TTC TTG CTG CAA CTT GGA GTG 192 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val 50 55 CCA GTA AAT GAA AAA GAC GAT GCA GGT TGG TCT CCT CTT CAT ATT GCT 240 Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala 65 70 75 GCT TCC GCT GGC CGG GAT GAG ATT GTA AAA GCC CTT CTG ATA AAA GGG 288 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly 85 90 95 GCA CAA GTG AAT GCC GTC AAT CAG AAT GGC TGC ACG GCC CTT CAT TAT 336 Ala Gln Val Asp Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr 100 105 GCA GCT TCC AAG AAT AGG CAT GAG ATT GCT GTT ATG TTA CTA GAA GGT 384 Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly GGG GCT AAT CCA GAT GCT AAG AAC CAT TAT GAT GCT ACA GCA ATG CAC 432 Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His 130 135 CGG GCA GCC AAG GGT AAC TTG AAG ATG GTT CAT ATC CTT CTG TTC 480 Arg Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe 145 150 155 160 TAC AAA GCA TCC ACA AAC ATC CAA GAT ACT GAG GGT AAC ACT CCT CTA 528 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu 165 170 CAC TTA GCC TGT GAT GAG GAG AGA GTG GAA GAA GCA AAA TTG CTG GTG 576 His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val

185

190

180

ACC	CAA	GGA	GCA	AGT	ATT	TAC	ATT	GAA	AAT	AAG	GAA	GAA	AAG	ACA	CCG	624
Thr	Gln	Gly	Ala	Ser	Ile	Tyr	Ile	Glu	Asn	Lys	Glu	Glu	Lys	Thr	Pro	
		195					200					205				
CTG	CAA	GTC	GCQ	AAA	GGG	GGC	CTG	GGT	TTA	ATA	CTC	AAA	AGA	ATC	GCA	672
Leu	Gln	Val	Ala	Lys	Gly	Gly	Leu	Gly	Leu	Ile	Leu	Lys	Arg	Ile	Ala	
	210			\		215					220					
GAA	AGT	GAA	GAG	фт	TCT	ATG	TAG									720
Glu	Ser	Glu	Glu	Ala	Ser	Met										
225				/	230											
SEQ	ID	NO:	: 6													
	uen			th:	2	31										
_	uen		_			io a	cid									
Top	olo	gy:	Li	nea	r											
Mol	ecu:	lar	Тур	e:	Pro	otai	n									
Seq	uen	ce														
Met	Glu	Gly	Суз	Val	Ser	Asn	Leu	Met	Val	Cys	Asn	Leu	Ala	Tyr	Asn	
1				5					10					15		
Gly	Lys	Leu	Asp	Glu	Leu	Lys	Glų	Ser	Ile	Leu	Ala	Asp	Lys	Ser	Leu	
			20				1	25					30			
Ala	Thr	Arg	Thr	Asp	Gln	Asp	Ser	Arg	Thr	Ala	Leu	His	Trp	Ala	Cys	
		35					40	•				45				
Ser	Ala	Gly	His	Thr	Glu	Ile	Val	Glu	Phe	Leu	Leu	Gln	Leu	Gly	Val	
	50					55		``			60					
	Val	Asn	Glu	Lys	Asp	Asp	Ala	Gly	Trp.	Ser	Pro	Leu	His	Ile	Ala	
65					70				,	75					80	
Ala	Ser	Ala	Gly	Arg	Asp	Glu	Ile	Val	Lys \	Ala	Leu	Leu	Ile	Lys	Gly	
				85					90,	\				95		
Ala	Gln	Val		Ala	Val	Asn	Gln		Gly	Cys	Thr	Ala		His	Tyr	
_			100					105		,			110			
Ala	Ala		Lys	Asn	Arg	His		Ile	Ala	Val	Met		Leu	Glu	Gly	
		115	_			_	120			, ·	λ.	125				
GTA		Asn	Pro	Asp	Ala		Asn	His	Tyr	Asp	Ì	Thr	Ala	Met	His	
λ	130	71 -	71 -	T	C1	135	T -	7	M- :	77- 7	140	~ 77 -	T	T =:	DF -	
_	wra	wTg	wra	тĀг	_	ASN	Leu	тĀг	Met		uls	ттө	теп	теп		
145	Lare	Δ Ι ~	802	ጥ ኮ ~	150	T10	C1 ~	λ c∽	Th∽	155 Glu	G1	A c ~	ሞሎ∽	Dro	160	
TAT	пÃа	VIG	Ser	165	Vall	116	GIII	vab	Thr 170	GIU	GTĀ	Lan	THE	175	Teu	
				- 00					± , 0					±,5		

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val

180 185

Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro

195 200 205

Leu Gln Val Afa Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Val

210 \ 215 220

230

Glu Ser Glu Glu Ala Ser Met

225

\

SEQ ID NO: 7

Sequence Length: 15

Sequence Type: Amino acid

Topology: Linear

Molecular Type: Peptide

Sequence

Met Glu Gly Cys Val Ser Asn Leu Met Val Cys Asn Leu Ala Tyr

1 5 \ 10 15

SEQ ID NO: 8

Sequence Length: 20

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CCTGTCGCT TTACCTCCCCA

SEQ ID NO: 9

Sequence Length: 20

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TACCTCCCCA CACACAGATT

20

20